

# FIGURE 1

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

FOI 280-2984450

GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACTGT  
GTTGAAGGGTGTCTTTTTTTCTTTTAAATGTAATACCTCCTCATCTTTTCTTCTTACACAGTG  
TCTGAGAACATTTACATTATAGATAAGTAGTACATGGTGGATAACTTCTACTTTTAGGAGGA  
CTACTCTCTTCTGACAGTCCTAGACTGGTCTTCTACACTAAGACACCATGAAGGAGTATGTG  
CTCCTATTATTCTGGCTTTGTGCTCTGCCAAACCCTTCTTTAGCCCTTCACACATCGCACT  
GAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATGATG  
ATGATGATGATGAGGACAACTCTCTTTTTTCCAACAAGAGAGCCAAGAAGCCATTTTTTTTCCA  
TTTGATCTGTTTCCAATGTGTCCATTTGGATGTCAGTGCTATTACGAGTTGTACATTGCTC  
AGATTTAGGTTTGACCTCAGTCCCAACCAACATTCCATTTGATACTCGAATGCTTGATCTTC  
AAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTTAAAGGACTCACTTCACTTTATGGT  
CTGATCCTGAACAACAACAAGCTAACGAAGATTCACCCAAAAGCCTTTCTAACCACAAAGAA  
GTTGCGAAGGCTGTATCTGTCCCAATCAACTAAGTGAAATACCACTTAATCTTCCCAAAT  
CATTAGCAGAACTCAGAATTCATGAAAATAAAGTTAAGAAAATACAAAAGGACACATTCAA  
GGAATGAATGCTTTACACGTTTTTGAAATGAGTGCAAACCCTCTTGATAATAATGGGATAGA  
GCCAGGGGCATTTGAAGGGGTGACGGTGTTCCATATCAGAATTGCAGAAGCAAACTGACCT  
CAGTTCCTAAAGGCTTACCACCAACTTTATTGGAGCTTCACTTAGATTATAATAAAATTTCA  
ACAGTGGAACCTTGAGGATTTTAAACGATACAAAGAACTACAAAGGCTGGGCCTAGGAAACAA  
CAAAATCACAGATATCGAAAATGGGAGTCTTGCTAACATACCACGTGTGAGAGAAATACATT  
TGGA AAAACAATAAACTAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATA  
ATCTTCCTTCATTCTAATTCAATTGCAAGAGTGGGAGTAAATGACTTCTGTCCAACAGTGCC  
AAAGATGAAGAAATCTTTATACAGTGCAATAAGTTTATTCAACAACCCGGTGAAATACTGGG  
AAATGCAACCTGCAACATTTCTGTTGTGTTTTGAGCAGAATGAGTGTTTCAGCTTGGGAACCTT  
GGAATGTAATAATTAGTAATTGGTAATGTCCATTTAATATAAGATTCAAAAATCCCTACATT  
TGGAATACTTGAACTCTATTAATAATGGTAGTATTATATATACAAGCAAATATCTATTCTCA  
AGTGGTAAGTCCACTGACTTATTTTATGACAAGAAATTTCAACGGAATTTTGCCAACTATT  
GATACATAAGGGGTGAGAGAAACAAGCATCTATTGCAGTTTCCTTTTTTGCGTACAAATGAT  
CTTACATAAATCTCATGCTTGACCATTCCCTTTCTTCATAACAAAAAAGTAAGATATTCCGTA  
TTTAACACTTTGTTATCAAGCACATTTTAAAAAGAACTGTACTGTAAATGGAATGCTTGACT  
TAGCAAAATTTGTGCTCTTTCAATTTGCTGTTAGAAAAACAGAATTAACAAAGACAGTAATGT  
GAAGAGTGCATTACACTATTCTTATTCTTTAGTAACTGGGTAGTACTGTAATATTTTTAAT  
CATCTTAAAGTATGATTTGATATAATCTTATTGAAATTACCTTATCATGTCTTAGAGCCCGT  
CTTTATGTTTTAAACTAATTTCTTAAATAAAGCCTTCAGTAAATGTTTATTACCAACTTGA  
TAAATGCTACTCATAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTTTAATTATT  
ACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTTCATAAAATCTGTAACTCGCATTTT  
AATGATCCGCTATTATAAGCTTTTAATAGCATGAAAATTGTTAGGCTATATAACATTGCCAC  
TTCAACTCTAAGGAATATTTTTGAGATATCCCTTTGGAAGACCTTGCTTGGAAGAGCCTGGA  
CACTAACAATTCTACACCAAATTGTCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAA  
CACATCTAGTATAACTGAATAAGCAGAGCATCAAATTAAACAGACAGAAACCGAAAGCTCTA  
TATAAATGCTCAGAGTTCTTTATGTATTTCTTATTGGCATTCAACATATGTAAAATCAGAAA  
ACAGGGAAATTTTCATTAAAAATATTGGTTTGAAAT

## FIGURE 2

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392

<subunit 1 of 1, 379 aa, 1 stop

<MW: 43302, pI: 7.30, NX(S/T): 1

MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDEDNSLFPTREPR  
SHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL  
TSLYGLILNNNKLTKIHPKAFLTTKKLRLLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQ  
KDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD  
YNKISTVELEDFKRYKELQRLGLGNNKITDIENGLANIIPRVREIHLENNKLKKIPSGLPPEL  
KYLQIIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSV  
QLGNFGM

### Signal sequence.

amino acids 1-15

### N-glycosylation site.

amino acids 281-285

### N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

### Leucine zipper pattern.

amino acids 154-176

APPROVED BY DRAFTSMAN	O.G. FIG.	SUBCLASS
	CLASS	

101 E80" 2984650

# FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGCCCCGSGCACCAGCCCCGGCCCCGGCCCTCCGCCCTCCGCACTCGCGCCTCC  
 CTCCCTCCGCCCGCTCCCGCGCCCTCTCCCTCCCTCTCCCCAGCTGTCCCGTTTCGCGTCATGCCGAGCCTCCC  
 GGCCCCGCGCGCCCCGCTGCTGCTCCTCGGGCTGCTGCTGCTCGGCTCCCGGCCGGCCCCGCGCGCCGGCCCCAGA  
 GCCCCCGTGTGCTGCCCATCCGTTCTGAGAAGGAGCCGCTGCCCGTTTCGGGGAGCGGCAGGCTGCACCTTCGGCGG  
 GAAGGTCTATGCCTTGACGAGACGTGGCACCCGGACCTAGGGCAGCCATTTCGGGGTGATGCGCTGCGTGTGCTGTG  
 CGCTGCGAGGCGCCTCAGTGGGGTTCGCCGTACCAGGGGCCCTGGCAGGGTTCAGCTGCAAGAACATCAAACCAGA  
 GTGCCAACCCCCGGCCTGTGGGCAGCCGCGCCAGCTGCCGGGACACTGCTGCCAGACCTGCCCCAGGAGCGCAG  
 CAGTTCGGAGCGGCAGCCGAGCGGCCTGTCTTCGAGTATCCGCGGGACCCGGAGCATCGCAGTTATAGCGACCG  
 CGGGGAGCCAGGCGCTGAGGAGCGGGCCCCGTGGTGACGGCCACACGGACTTCGTGGCGCTGCTGACAGGGCCGAG  
 GTCGAGGCGGTGGCACGAGCCCCGAGTCTCGCTGCTGCGCTCTAGCCTCCGCTTCTCTATCTCCTACAGGCGGCT  
 GGACCGCCCTACCAGGATCCGCTTCTCAGACTCCAATGGCAGTGTCTGTTTGAGCACCCCTGCAGCCCCACCCA  
 AGATGGCCTGGTCTGTGGGGTGTGGCGGGCAGTGCCCTCGTTGTCTCTGCGGCTCCTTAGGGCAGAACAGCTGCA  
 TGTGGCACTTGTGACACTCACTCACCTTTCAGGGGAGGTCTGGGGCCCTCTCATCCGGCACCGGGCCCTGGCTGC  
 AGAGACCTTCAGTGCCATCCTGACTCTAGAAGGCCCCCACAGCAGGGCGTAGGGGGCATCACCTGCTCACTCT  
 CAGTGACACAGAGGACTCCTTGCACTTTTTTGTGCTCTTCCGAGGGCTGCTGGAACCCAGGAGTGGGGGACTAAC  
 CCAGGTTCCCTTGAGGCTCCAGATTCTACACCAGGGGCGAGTACTGCGAGAACTTCAGGCCAATGTCTCAGCCCCA  
 GGAACCAGGCTTTGCTGAGGTGCTGCCAACCTGACAGTCCAGGAGATGGACTGGCTGGTGTGCTGGGGGAGCTGCA  
 GATGGCCCTGGAGTGGGCAGGCAGGCCAGGGCTGCGCATCAGTGGACACATTGCTGCCAGGAAGAGCTGCGACGT  
 CCTGCAAAGTGTCTTTGTGGGGCTGATGCCCTGATCCAGTCCAGACGGGTGCTGCCGGCTCAGCCAGCCTCAC  
 GCTGCTAGGAAATGGCTCCCTGATCTATCAGGTGCAAGTGGTAGGGACAAGCAGTGAGGTGGTGGCCATGACACT  
 GGAGACCAAGCCTCAGCGGAGGGATCAGCGCACTGTCTGTCACATGGCTGGACTCCAGCCAGGAGGACACAC  
 GGCCGTGGGTATCTGCCCTGGGCTGGGTGCCCCAGGGGCTCATATGCTGCTGCGAGAATGAGCTCTTCTGAACGT  
 GGGCACCAAGGACTTCCAGACGGAGAGCTTCGGGGGCAGTGCGCTGCCCTGCCCTACTGTGGGCATAGCGCCCG  
 CCATGACACGCTGCCCGTGCCCTAGCAGGAGCCCTGGTGCTACCCCTGTGAAGAGCCAAGCAGCAGGGGCACGC  
 CTGGCTTTCTTGATACCCACTGTACCTGCACTATGAAGTGCTGCTGGCTGGGCTTGGTGGCTCAGAACAAGG  
 CACTGTCACTGCCCCACCTCCTTGGGCCTCCTGGAACGCCAGGGCCTCGGCGGCTGCTGAAGGGATTCTATGGCTC  
 AGAGGCCCAGGGTGTGGTGAAGGACCTGGAGCCGGAAGTGTGCGGCACCTGGCAAAAGGCATGGCCTCCCTGAT  
 GATCACCAAGGGTAGCCCCAGAGGGGAGCTCCGAGGGCAGGTGCACATAGCCAACCAATGTGAGGTGGCGG  
 ACTGCGCTGGAGGCGGCGGGGCCGAGGGGGTGCGGGCGCTGGGGGCTCCGGATACAGCCTCTGCTGCGCCGCC  
 TGTGGTGCCTGGTCTCCCGGCCCTAGCGCCCGCCAAACCTGGTGGTCTGGGCGGCCCCGAGACCCCAACACATG  
 CTTCTTCGAGGGGCGAGCAGCGCCCCACGGGGCTCGCTGGGCGCCCAACTACGACCCGCTCTGCTCACTCTGCAC  
 CTGCCAGAGACGAACGGTGATCTGTGACCCGGTGGTGTGCCACCCGCCAGCTGCCCAACCCGGTGCAGGCTCC  
 CGACCACTGCTGCCCTGTTTGCCCTGAGAAACAAGATGTCAGAGACTTGCCAGGGCTGCCAAGGAGCCGGGACCC  
 AGGAGAGGGCTGCTATTTTGATGGTGACCGGAGCTGGCGGGCAGCGGTACGCGGTGGCACCCCGTTGTGCCCCC  
 CTTTGGCTTAATTAAGTGTGCTGTCTGCACCTGCAAGGGGGGCACTGGAGAGGTGCACTGTGAGAAGGTGCAGTG  
 TCCCCGGCTGGCCTGTGCCAGCCTGTGCGTGTCAACCCACCGACTGCTGCAAACAGTGTCCAGTGGGGTCGGG  
 GGCCACCCCACTGAGGAGGACCCCATGCAGGCTGATGGGCCCCGGGGCTGCCGTTTTGCTGGGCAGTGGTTCCC  
 AGAGAGTCAGAGCTGGCACCCCTCAGTGCCCCCTTTTGGAGAGATGAGCTGTATCACTGCAGATGTGGGGCAGG  
 GGTGCCTCACTGTGAGCGGGATGACTGTTCACTGCCACTGTCTGTGGCTCGGGGAAGGAGAGTCGATGCTGTTC  
 CCGCTGCACGGCCACCGCGGCCCCCCAGAGACCAGAACTGATCCAGAGCTGGAGAAAGAAGCCGAAGGCTCTTA  
 GGGAGCAGCCAGAGGGCCAAGTGACCAAGAGGATGGGGCCTGAGCTGGGGAAGGGGTGGCATCGAGGACCTTCTT  
 GCATTCTCCTGTGGGAAGCCAGTGCCCTTTGCTCCTGTCTCTGCTCTACTCCCACCCCACTACCTCTGGGAA  
 CCACAGCTCCACAAGGGGGAGAGGCAGCTGGGCCAGACCGAGGTACAGCCACTCCAAGTCCCTGCCCTGCCACCC  
 TCGGCCTCTGTCTGGAAGCCCCACCCCTTTCTCCTGTACATAATGTCACTGGCTTGTGGGATTTTTAATTTA  
 TCTTCACTCAGCACCAAGGGCCCCGACACTCCACTCCTGCTGCCCTGAGCTGAGCAGAGTCATTATTGGAGAG  
 TTTTGTATTTATTAAACATTTCTTTTTCAGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

APPROVED	O.G. FIG.	
	CLASS	SUBCLASS
BY	DRAFTSMAN	

004456-03401

## FIGURE 4

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

MPSLPAPPAPLLLLLGLLLLGSRPARGAGPEPPVLPPIRSEKEPLPVRGAAGCTFGGKVYALDE  
 TWHPD LGQPF GVMRCVLCACEAPQWGRRTRGPGRVSCNKKPECPTPACGQPRQLPGHCCQT  
 CPQERSSSERQPSGLSFEYPRDPEHRSYSDRGEPGAEEERARGDGHTDFVALLTGPRSQAVAR  
 ARVSLRLRSSLRFSISYRRLDRPTRIRFSDSNGSVLFEHPAAPTQDGLVCGVWRAVPRLSLRL  
 LRAEQLHVALVTLTTHPSGEVWGPLIRHRALAAETFSAILTLEGPPQQGVGGITLLTSLDTE  
 SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQGQLLRELQANVSAQEPGFAEVLPLNLTVQEMD  
 WLVLGELQMALEWAGRPLRISGHIAARKSCDVLQSVLCGADALIPVQTGAAGSASLTLLGN  
 GSLIYQVQVVGTSSEVVAMTLETKPQRRDQRTVLCHMAGLQPGGHTAVGICPGLGARGAAML  
 LQNELFLNVGTDKDFPDGELRGHVAALPYCGHSARHDTLPVPLAGALVLPVKSQAAGHAWLS  
 LDTHCHLHYEVLLAGLGGSEQGTVAHLLGPPGTPGPRRLKGFYGYSEAQGVVKDLEPELLR  
 HLAKGMA SLMITTKGSPRGELRGQVHIANQCEVGGLRLEAAGAEGVRALGAPDTASAAPPVV  
 PGLPALAPAKPGGPGRPRDPNTCFFEGQQRPHGARWAPNYDPLCSLCTCQRRTVICDPVVC  
 PPSCPHPVQAPDQCCPVCPEKQDVRDLPLGLPRSRDPGEGCYFDGDRSWRAAGTRWHPVVPF  
 GLIKCAVCTCKGGTGEVHCEKVQCPRLACAQPV RVNPTDCCCKQCPVGSGAHPQLGDPMQADG  
 PRGCRFAGQWFPESQSWHPSVPPFGEMSCITCRGAGVPHCERDDCSLPLSCGSGKESRCCS  
 RCTAHRPPETRTDPELEKEAEGS

**Signal sequence.**

amino acids 1-23

**N-glycosylation sites.**

amino acids 217-221, 351-355, 365-369, 434-438

**Tyrosine kinase phosphorylation sites.**

amino acids 145-153, 778-786

**N-myristoylation sites.**

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,  
 390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,  
 576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,  
 905-911

**Amidation site.**

amino acids 87-91

**Cell attachment sequence.**

amino acids 165-168

**Leucine zipper pattern.**

amino acids 315-337

O.G. FIG.	SUBCLASS
	CLASS
APPROVED BY	DRAFTSMAN

T07E30-29844650

# FIGURE 5

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

094435-0310

GGCGGAGCAGCCCTAGCCGCCACCGTCGCTCTCGCAGCTCTCGTCGCCACTGCCACCGCCGCCGCGTCACTGCC  
 TCCTGGCTCCGGCTCCCGCGCCCTCCCGGCCGGCCATGAGCCCCCGCGCCCGAGGCGCCCGGTGCGCAGCTGC  
 TGCCCCGCGTGGCCCTGCTGCTGCTGCTGCTCGGAGCGGGGCCCCGAGGAGCTCCCTGGCCAACCCGGTGCCCCG  
 CCGCGCCCTTGTCTGCGCCCGGGCCGTGCGCCGCGCAGCCCTGCCGGAATGGGGGTGTGTGCACCTCGCGCCCTG  
 AGCCGGACCCGAGCACCCGGCCCCCGCGCGAGCCTGGCTACAGCTGCACCTGCCCGCCGGGATCTCCGGCG  
 CCAACTGCCAGCTTGTTCAGATCCTTGTGCCAGCAACCCTTGTACCATGGCAACTGCAGCAGCAGCAGCAGCA  
 GCAGCAGCGATGGCTACCTCTGCATTTGCAATGAAGGCTATGAAGGTCCCAACTGTGAACAGGCACTTCCCAGTC  
 TCCCAGCCACTGGCTGGACCGAATCCATGGCACCCCGACAGCTTCAGCCTGTTCTCTGCTACTCAGGAGCCTGACA  
 AAATCCTGCCTCGCTCTCAGGCAACGGTGACACTGCCCTACCTGGCAGCCGAAAACAGGGCAGAAAGTTGTAGAAA  
 TGAAATGGGATCAAGTGGAGGTGATCCAGATATTGCCTGTGGGAATGCCAGTTCTAACAGCTCTGCGGGTGGCC  
 GCCTGGTATCCTTTGAAGTGCCACAGAACACCTCAGTCAAGATTCCGCAAGATGCCACTGCCTCACTGATTTTGC  
 TCTGGAAGGTACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAGTGTGACCCCCCTTCAGGCTT  
 CAGGGGACTGGTCTCTCGAGGAGATGCTCGCCTTGGGGAATAATCACTTTATTGGTTTTGTGAATGATTCTG  
 TGACTAAGTCTATTGTGGCTTTGCGCTTAACTCTGGTGGTGAAGGTGAGCACCTGTGTGCCGGGGGAGAGTCAG  
 CAAATGACTTGGAGTGTTCAGGAAAAGGAAAATGCACCACGAAGCCGTGAGAGGCAACTTTTTCTGTACCTGTG  
 AGGAGCAGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAACCGGAGCT  
 GTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCTGGTTATACTGGAGAGCTTT  
 GCCAGTCCAAGATTGATTACTGCATCCTAGACCCATGCAGAAATGGAGCAACATGCATTTCCAGTCTCAGTGGAT  
 TCACCTGCCAGTGTCCAGAAGGATACTTCGGATCTGCTTGTGAAGAAAAGGTGGACCCCTGCGCCTCGTCTCCGT  
 GCCAGAACACGGCACCTGCTATGTGGACGGGGTACACTTTACCTGCAACTGCAGCCCGGGCTTCACAGGGCCGA  
 CCTGTGCCCAGCTTATTGACTTCTGTGCCCTCAGCCCTGTGCTCATGGCACGTGCCGAGCGTGGGCACCAGCT  
 ACAAATGCCTCTGTGATCCAGGTTACCATGGCCTCTACTGTGAGGAGGAATATAATGAGTGCCTCTCCGCTCCAT  
 GCCTGAATGCAGCCACCTGCAGGGACCTCGTTAATGGCTATGAGTGTGTGTGCCTGGCAGAATACAAAGGAACAC  
 ACTGTGAATTGTACAAGGATCCCTGCGCTAACGTGAGTGTCTGAACGGAGCCACCTGTGACAGCGACGGCCTGA  
 ATGGCACGTGCATCTGTGCACCCGGGTTTACAGGTGAAGAGTGCAGCATTGACATAAATGAATGTGACAGTAACC  
 CCTGCCACCATGGTGGGAGCTGCCTGGACAGCCCAATGGTTATAACTGCCACTGCCCGCATGGTTGGGTGGGAG  
 CAACTGTGAGATCCACCTCCAATGGAAGTCCGGGCACATGGCGGAGAGCCTCACCACATGCCACGGCACTCCC  
 TCTACATCATCATTGGAGCCCTCTGCGTGGCCTTCATCCTTATGCTGATCATCCTGATCGTGGGATTGTCCGCA  
 TCAGCCGATTGAATACCAGGGTTCTTCCAGGCCAGCCTATGAGGAGTTCTACAAGTCCCGCAGCATCGACAGCG  
 AGTTACAGCAATGCCATTGCATCCATCCGGCATGCCAGGTTTGGAAAGAAATCCCGGCCTGCAATGTATGATGTGA  
 GCCCCATCGCCTATGAAGATTACAGTCTGATGACAAACCCTTGGTCACACTGATTAAACTAAAGATTTGTAAT  
 CTTTTTTTGGATTATTTTTCAAAAAGATGAGATACTACACTCATTAAATATTTTTAAGAAAATAAAAAGCTTAA  
 GAAATTTAAATGCTAGCTGCTCAAGAGTTTTAGTAGAATATTTAAGAACTAATTTCTGCAGCTTTTAGTTG  
 GAAAAAATATTTTAAAAACAAAATTTGTGAAACCTATAGACGATGTTTTAATGTACCTTCAGCTCTCTAACTGT  
 GTGCTTCTACTAGTGTGTGCTCTTTTCACTGTAGACACTATCACGAGACCCAGATTAATTTCTGTGGTTGTTACA  
 GAATAAGTCTAATCAAGGAGAAAGTTTCTGTTTGACGTTTGAAGTCTGAAATGTTTGGTTTGTGGA  
 GTAACGTAGCATATGATGTATAATAGAGTATACCCGTTACTTAAAAAGAGTCTGAAATGTTTGGTTTGTGGA  
 AGAACTAGTTAAATTTACTATTCCCTAACCCGAATGAAATTAGCCTTTGCCTTATTCTGTGCATGGGTAAAGTAAC  
 TTATTTCTGCACTGTTTTTGTGAACTTTGTGGAACATTCTTTTCAGTTTGTTTTTGTCAATTTTCGTAACAGTCG  
 TCGAACTAGGCCTCAAAAACATACGTAACGAAAAGGCCTAGCGAGGCAAAATCTGATTGATTTGAATCTATATTT  
 TTCTTTAAAAAGTCAAGGGTTCTATATTGTGAGTAAATTAATTTACATTTGAGTTGTTTGTGCTAAGAGGTAG  
 TAAATGTAAGAGAGTACTGGTTCCTTCAGTAGTGAGTATTTCTCATAGTGAGCTTTATTTATCTCCAGGATGTT  
 TTTGTGGCTGATTTGATTGATATGTGCTTCTTCTGATTCTTGCTAATTTCCAACCATATTGAATAAATGTGATC  
 AAGTCA

## FIGURE 6

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQLLPALALLLLLLLGAGPRGSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSR  
PEPDPQHPAPAGEPGYSCTCPAGISGANCLVADPCASNPCHHGNCSSSSSSSSSDGYLCICN  
EGYEGPNCEQALPSLPATGWTESMAPRQLQPVVPATQEPDKILPRSQATVTLPTWQPKTGQKV  
VEMKWDQVEVIPDIACGNASSNSSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGFQ  
QCSLIDGRSVTPLQASGGLVLLLEMLALGNNHFIGFVNDVTKSIVALRLTLVVKVSTCVPG  
ESHANDLECSGKGKCTTKPSEATFSCCTEEQYVGTFCEEYDACQRKPCQNNASCIDANEKQD  
GSNFTCVCLPGYTGELCQSKIDYICILDPCRNGATCISSLSGFTCQCPEGYFGSACEEKVDPC  
ASSPCQNNGTCTYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCRSVGTSTYKCLCDPG  
YHGLYCEEEYNECLSAAPCLNAATCRDLVNGYECVCLAELYKGDPCANVSCNLGATC  
DSDGLNGTCICAPGFTGEECDIDINECDSPNCHHGGSCLDQPNGYNCHCPHGWVGANCEIHL  
QWKS GHMAESLTNMPRHSLYIIIGALCVAFILMLIILIVGICRISRIEYQGSSRPAYEEFYN  
CRSIDSEFSNAIASIRHARFGKKS RPAMYDVSP IAYEDYSPDDKPLVTLIKTKDL

**Signal sequence.**

amino acids 1-28

**Transmembrane domain.**

amino acids 641-660

**N-glycosylation sites.**

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,  
375-379, 442-446, 549-553, 564-568

**Glycosaminoglycan attachment site.**

amino acids 320-324

**Tyrosine kinase phosphorylation sites.**

amino acids 490-498, 674-682

**N-myristoylation sites.**

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,  
373-379, 449-455, 480-486, 562-568, 565-571

**Amidation site.**

amino acids 702-706

**Aspartic acid and asparagine hydroxylation site.**

amino acids 520-532, 596-608

**EGF-like domain cysteine pattern signatures.**

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,  
491-503, 529-541, 567-579, 605-617

APPROVED	O.G. FIG.	
	CLASS	SUBCLASS
BY	DRAFTSMAN	

T01E80-29044650

## FIGURE 7

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA  
CCCCCCTTTCAGGCTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA  
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT  
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTT  
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCTGTACCTGTGAGGAGC  
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC  
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCC  
TGGTTATACTGGAGAGCTTTGCCAACC GA ACTGAGATTGGAGCGAACGACCTACACCGA ACT  
GAGATAGGGGAG

APPROVED BY DRAFTSMAN	O.G. FIG.	SUBCLASS
	CLASS	

FOI b7D b7C b7E b7F b7G b7H b7I b7J b7K b7L b7M b7N b7O b7P b7Q b7R b7S b7T b7U b7V b7W b7X b7Y b7Z

## FIGURE 8

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA  
CCCCCCTTTCAGGCCTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA  
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT  
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTT  
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCTGTACCTGTGAGGAGC  
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC  
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCC  
TGGTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT  
GAGATAGGGGAG

APPROVED	OG. FIG.	SUBCLASS
BY	CLASS	
DRAFTSMAN		

0944862-083401



# FIGURE 9

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

0044660

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAG  
 GGGGGGGCAGAGCCCTCACCACGCTGGGCGCCCCCAGAGCCCACACCATGCCGGGCACCTAC  
 GCTCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGGCCCT  
 GATGCGGGACTTCCCGCTCGTGGACGGCCACAACGACCTGCCCCCTGGTCCTAAGGCAGGTTT  
 ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTTAGCTACGGCCAGACCAGCCTGGAC  
 AGGCTTAGAGATGGCCTCGTGGGCGCCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA  
 GGACCGGGATGCCCTGCGCCTCACCCCTGGAGCAGATTGACCTCATACGCCGCATGTGTGCCT  
 CCTATTCTGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC  
 TGCCTCATCGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT  
 CTACATGCTGGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCCTGGGCAGAGA  
 GCTCCGCTAAGGGCGTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAG  
 AAGGTGGTGGCAGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGC  
 TGTGGCACGGCGGGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGCTGCCC  
 GGGGTGTGTGCAACAGTGCTCGGAATGTTCTGATGACATCCTGCAGCTTCTGAAGAAGAAC  
 GGTGGCGTCTGATGGTGTCTTTGTCCATGGGAGTAATACAGTGCAACCCATCAGCCAATGT  
 GTCCACTGTGGCAGATCACTTCGACCACATCAAGGCTGTCATTGGATCCAAGTTCATCGGGA  
 TTGGTGGAGATTATGATGGGGCCGGCAAATTCCTCAGGGGCTGGAAGACGTGTCCACATAC  
 CCGGTCCTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTT  
 TCGTGGAACCTGCTGCGGGTCTTCAGACAAGTGGAAGAGGTACAGGAAGAAAACAAATGGC  
 AAAGCCCCCTTGAGGACAAGTTCCCGGATGAGCAGCTGAGCAGTTCCTGCCACTCCGACCTC  
 TCACGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACTCACTGAGATTCCCATACA  
 CTGGACAGCCAAGTTACCAGCCAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAG  
 TCCTTGCAAGTTGTGGCCACCTTCCCAGTCCTTATTCTGTGGCTCTGATGACCCAGTTAGTCC  
 TGCCAGATGTCACTGTAGCAAGCCACAGACACCCACAAAGTTCCCCTGTTGTGCAGGCACA  
 AATATTTCTGAAATAAATGTTTTGGACATAG

# FIGURE 10

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595

<subunit 1 of 1, 433 aa, 1 stop

<MW: 47787, pI: 6.11, NX(S/T): 5

MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG  
 QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRRMCASYSLELVTSKALND  
 TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL  
 TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ  
 LLKKNGGVVMVSLSMGVIQCNP SANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE  
 DVSTYPVLIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS  
 CHSDLSRLRQRQSLTSGQELTEIPHWAKLPKWSVSESSPHMAPVLAVVATFPVLILWL

## N-glycosylation sites.

amino acids 58-62, 123-127, 182-186, 273-277

## N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

## Renal dipeptidase active site.

amino acids 134-157

O.G. FIG.		SUBCLASS
APPROVED	BY	DRAFTSMAN

00944862 083401

# FIGURE 11

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

AAAACCTATAAATATTCCGGATTATTCATACCGTCCCACCATCGGGCGCGGATCCGCGGCCG  
 CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCCAGCA  
 CCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGATGCGGGACTTCCCGCTCGTGGACGGCCAC  
 AACGACCTGCCCCCTGGTCCTAAGGCAGGTTTACCAGAAAGGGCTACAGGATGTAAACCTGCG  
 CAATTTTCAGCTACGGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGGCGCCCAGT  
 TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCGGGATGCCCTGCGCCTCACCTGGAG  
 CAGATTGACCTCATACGCCGCATGTGTGCCTCCTATTCTGAGCTGGAGCTTGTGACCTCGGC  
 TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCATCGGTGTAGAGGGTGGCCACTCGC  
 TGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCTGGGAGTGCCTACCTGACGCTC  
 ACCCACACCTGCAACACACCCTGGGCAGAGAGCTCCGCTAAGGGCGTCCACTCCTTCTACAA  
 CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGCAGAAATGAACCGCCTGGGCA  
 TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAGTGTACAG  
 GCACCTGTGATCTTCTCCCACTCGGCTGCCCCGGGGTGTGTGCAACAGTGCTCGGAATGTTCC  
 TGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTTGTCCATGG  
 GAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTTCGACCACATC  
 AAGGCTGTCATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGATGGGGCCGGCAAATT  
 CCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCCTGATAGAGGAGTTGCTGAGTCGTG  
 GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTCGTGGAACCTGCTGCGGGTCTTCAGACAA  
 GTGGAAAAGGTACAGGAAGAAAAACAAATGGCAAAGCCCCTTGAGGACAAGTTCGCGGATGA  
 GCAGCTGAGCAGTTCCTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACAGAGTCTGACTT  
 CAGGCCAGGAACTCACTGAGATTCCCATACTGGACAGCCAAGTTACCAGCCAAGTGGTCA  
 GTCTCAGAGTCCTCCCCCACCCTGACAAAACCTCACACATGCCACCGTGCCCAGCACCTGA  
 ACTCCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCCAAGGACACC

09044362 "083401

## FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872

><subunit 1 of 1, 446 aa, 0 stop

><NX(S/T): 5

MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG  
 QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALND  
 TQKLACCLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL  
 TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ  
 LLKKNNGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE  
 DVSTYPVLIEELLSRGWSEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS  
 CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHDPDKTHTCPPCPAPELLGGP  
 SVFLFPPKPKDT

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

T01E20 29944650



**FIGURE 14**

><SS.DNA38113

```
><subunit 1 of 1, 422 aa, 1 stop
```

><MW: 46302, pI: 9.42, NX(S/T): 6

MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVIS PQDPTLLIGSSLLATCSV

HGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSIL

AGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSCLKYKLRWYGQDNTCEE

YHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVTTDPPPDVHVS RVGG

LEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVDDVSNQTSCLAGLKP GTVYFVQ

LEDQLSVRWVSFFALREI...  
VRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLG

WLKKHAYCSNLSFRLYDQWRAWMQSHKTRNQDEGILPSGRRGTARGPAR

Signal sequence.

amino acids 1-30

Transmembrane domain.

amino acids 44-61

N-glycosylation sites.

N-glycosylation sites.  
amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 413-417

N-myristoylation sites.

N-myristoylation sites:  
amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,  
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

Amidation site.

amino acids 3-7, 79-83, 411-415

Growth factor and cytokines receptors family signature 2.

amino acids 325-331

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

0941045002101

# FIGURE 15

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

0944862-03101

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA  
 AAAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC  
 CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTTAA  
 GAGGAGAAAATCAGTCACCGGCGAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA  
 GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG  
 CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTCATACCTTTGT  
 GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG  
 GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA  
 CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGACATTTCTGGACTACAAA  
 GGCATTTCTTCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG  
 CTGGACATGTCTCGGTCCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTTGGA  
 TTTTATAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG  
 TCTGTGTCCTAATTTTCGTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA  
 CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG  
 ATTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCTGAGCGTTT  
 CCTGGCAGTTTTTAAACGAAAAATCAGTGTAAAGTTTGATGCAGTTATTGGATATAAAATGA  
 AAGCGCAATAAGCACCTAGTTTTCTGAAAACGATTTACCAGGTTTAGGTTGATGTCATCTA  
 ATAGTGCCAGAATTTAATGTTTGAACCTCTGTTTTTTCTAATTATCCCCATTTCTTCAATA  
 TCATTTTTGAGGCTTTGGCAGTCTTCATTTACTACCACTTGTTCTTTAGCCAAAAGCTGATT  
 ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA  
 CCAAAATGACTTTATTAAATAAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA  
 AATTTGTACCATAACCGTTTATTTAACATATATTTTATTTTGGATTGCACTTAAATTTGT  
 ATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA  
 TGAAGGACTATATCTAGTGGTATTTTACAATGAATATCATGAACTCTCAATGGGTAGGTTTC  
 ATCCTACCCATTGCCACTCTGTTTCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT  
 GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG  
 GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACTTAAAAAAA  
 AA  
 AA

## FIGURE 16

</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436

<subunit 1 of 1, 300 aa, 1 stop

<MW: 32964, pI: 9.52, NX(S/T): 1

MKFLLDILLLLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDSCNREDIYSSAKKVKAIEIGDVSILVNNAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

**Signal sequence.**

amino acids 1-19

**Transmembrane domain.**

amino acids 170-187

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 30-34, 283-287

**N-myristoylation sites.**

amino acids 43-49, 72-78, 122-128, 210-216

APPROVED BY	O.G. FIG.	
	CLASS	SUBCLASS
DRAFTSMAN		

101530 29944650



# FIGURE 17

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGACTG  
GGGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCACCAA  
CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACT  
GCGAGAGGACCCCGGCGTCCGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCCTGC  
TGCTCCTGGGCCTGGCGGCCGGCTCGCCCCCACTGGACGACAACAAGATCCCCAGCCTCTGC  
CCGGGGCACCCTGGCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCCGGGGCCG  
CGATGGCCGCGACGGCCGCGACGGCGCGCCCGGGGCTCCGGGAGAGAAAGGCGAGGGCGGGA  
GGCCGGGACTGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGAGGCGGGACCCGCGGGG  
CCCACCGGGCCTGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTC  
CGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCTTGCCCTTCGACCGCGTGCTGGTGAACG  
AGCAGGGACATTACGACGCCGTACCCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTAC  
TTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGA  
ATCCATTGCCTCTTTCTTCCAGTTTTTCGGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGG  
GGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTAC  
ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTTCTCCGGATTTCTGGTGTACTCCGA  
CTGGCACAGCTCCCCAGTCTTTGCTTAGTGCCCCACTGCAAAGTGAGCTCATGCTCTCACTCC  
TAGAAGGAGGGTGTGAGGCTGACAACCAGGTATCCAGGAGGGCTGGCCCCCTGGAATATT  
GTGAATGACTAGGGAGGTGGGGTAGAGCACTCTCCGTCCTGCTGCTGGCAAGGAATGGGAAC  
AGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACCA  
GAGGAGTGTGCTGTGCTGGCAAGTGTAAGTCCCCCAGTTGCTCTGGTCCAGGAGCCCACGGT  
GGGGTGCTCTCTTCTGCTCCTCTGCTTCTCTGGATCCTCCCCACCCCTCCTGCTCCTGGG  
GCCGGCCCTTTTCTCAGAGATCACTCAATAAACCTAAGAACCCTCATAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAA

APPROVED BY DRAFTSMAN	O.G. FIG.	SUBCLASS
	CLASS	

094156-083101

## FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592

><subunit 1 of 1, 243 aa, 1 stop

><MW: 25298, pI: 6.44, NX(S/T): 0

MRPLLVLALLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAP  
 GEKGEGRPGPLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLP  
 FDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWP  
 KPASLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

**Signal sequence.**

amino acids 1-15

**N-myristoylation sites.**

amino acids 11-17, 68-74, 216-222

**Cell attachment sequence.**

amino acids 77-80

APPROVED	CLASS	SUBCLASS
BY		
DRAFTSMAN		

094432 083101

# FIGURE 19

CTCTTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG  
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCAACAGACCCAT  
GCTGCATCCAGAGACCTCCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTTG  
GCACCACCTGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC  
CTGAACAGGAAGGAGAGTTTCTTGCTCCTCTCCCTGCACAACCGCCTGCGCAGCTGGGTCCA  
GCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAG  
CCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCCTG  
CAAGTGGGCTGGAACATGCAGCTGCTGCCCCGCGGGCTTGGCGTCCTTTGTTGAAGTGGTCAG  
CCTATGGTTTGCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAGTGTGCTCGCAACGCCA  
CCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGGCGGCAC  
CTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGTGCCTACTCCCCCGGAGGCAA  
CTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAGGGTGCCTGGTGTTCGCTCTGCA  
CAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGGCTCTGTGAGGTCCCC  
AGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGACGTCTCAACATCAGCACCTGCCACTG  
CCACTGTCCCCCTGGCTACACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGC  
ACGGCCGGTTCGGGAGGAGGAGTGCTCGTGCCTGTGTGACATCGGCTACGGGGGAGCCAG  
TGTGCCACCAAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT  
CATGGTGTCTTCAAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGCG  
GGGTGCTGGCCCAGATCAAGAGCCAGAAAGTGACAGGACATCCTCGCCTTCTATCTGGGCCGC  
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACCTTCTGGATCGGGCT  
CACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACCA  
GTTTTGCCTTTGGGCAGCCTGACAACCACGGGCTGGTGTGGCTGAGTGTGCCATGGGGTTT  
GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAAC  
CCGAAACCGTTACATCTGCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGGCCCAGGGTCCT  
GAGGCCTGACCACATGGCTCCCTCGCCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGC  
CCACCTGTCTGGAACAAGGGCCAGGTAAAGACCACATGCCTCATGTCCAAGAGGTCTCAGA  
CCTTGACAAATGCCAGAAGTTGGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTG  
AGTGTTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGA  
TGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAGGCTGCTCTCTTCCACCTGGCCCAGAC  
CCTGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCACGGGGTATTAAATTATGAATCAG  
CTGAAAAAAAAAAAAA

O.G. FIG.		SUBCLASS
APPROVED	BY	DRAFTSMAN

101530 2954660

## FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176

<subunit 1 of 1, 455 aa, 1 stop

<MW: 50478, pI: 8.44, NX(S/T): 2

MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEAPMAGALNRKESFLLLSLHNRLRSWV  
QPPAADMRRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV  
SLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSPGG  
NWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRLNISTCH  
CHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFHTCDLRIDGDC  
FMVSSEADTYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVTDSDFETRNFWIG  
LTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCK  
TRNRYICQFAQEHISRWGPGS

### Signal sequence.

amino acids 1-26

### Transmembrane domain.

amino acids 110-124

### N-glycosylation sites.

amino acids 144-148, 243-247

### cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 45-49

### N-myristoylation sites.

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,  
288-294, 331-337, 398-404

### Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 204-215

### EGF-like domain cysteine pattern signature.

amino acids 249-261, 280-292

### C-type lectin domain signature.

amino acids 417-442

APPROVED	O.G. FIG.	SUECLASS
BY	CLASS	
DRAFTSMAN		

T0TE80 2934466

APPROVED	O.G. F.G.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

09-16-2008 10:01

[illegible]

## FIGURE 22

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192

<subunit 1 of 1, 694 aa, 1 stop

<MW: 77400, pI: 9.54, NX(S/T): 6

MLLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLLQRLKTKPLMTEFSVKSTIIS  
 RYAFTTVSCRMLNRASEDQDIEFQMQUIPAAAFITNFTMLIGDKVYQGEITEREKKSGDRVKE  
 KRNKTTEENGEKGTEIFRASAVIPSKDKAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRLS  
 VDVNILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPPSTVINQNETFANIIFKPTVVQQAR  
 IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFLDSSASMVGTK  
 LRQTKDALFTILHDLRPQDRFSIIGFSNRIKVKDHLISVTPDSIRDGKVYIHHMSPTGGTD  
 INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKILNNTREAARGQVCIF  
 TIGIGNDVDFRLLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSV  
 QATKTLFPNYFNGSEIIAGKLVDRKLDHLHVEVTASNKKFIIKTDVPVRPQKAGKDV  
 TSPRPGGDGEGDTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTS  
 MKLRGPVPRMDGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKKQNKTKKRHGR  
 DGVFPLHHLGIR

**Signal sequence.**

amino acids 1-14

**N-glycosylation sites.**

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

**Glycosaminoglycan attachment sites.**

amino acids 213-217, 391-395

**N-myristoylation sites.**

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

APPROVED	C.G. FIG.	
	CLASS	SUBCLASS
BY	DRAFTSMAN	

107220-2934466

## FIGURE 23

CGGACGCGTGGGGTGCCCGACATGGCGAGTG TAGTGCTGCCGAGCGGATCCCAGTGTGCGGC  
GGCAGCGGCGGCGGCGGCGCCTCCCGGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCCGCGG  
CACTGATCCCCACAGGTGATGGGCAGAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGA  
GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTGAGCTACTGAA  
TCCCAACAGGCAGACCATTTATTTTCAAGGACTTCAGGCCTTTGAAGGACAGCAGGTTTCAGT  
TGCTGAATTTTTCTAGCAGTGAACCTCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAA  
GGAAGATACTTTTGCCAGCTCTATACCGATCCCCCACAGGAAAGTTACACCACCATCACAGT  
CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG  
AGATTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAAA  
GGGAACACAGAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC  
CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGATCTGCCAGGTGG  
AGCACCCTGCGGTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT  
CAAGTGACATTCAGATGACTTATCCTCTACAAGGCTTAACCCGGGAAGGGGACGCGCTTGA  
GTTAACATGTGAAGCCATCGGGAAGCCCCAGCCTGTGATGGTAACTTGGGTGAGAGTCGATG  
ATGAAATGCCTCAACACGCCGTACTGTCTGGGCCCAACCTGTTTCATCAATAACCTAAACAAA  
ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTA  
TATGCTGTATGTATACGATCCCCCACAACTATCCCTCCTCCCACAACAACCACCACCACCA  
CCACCACCACCACCACCACCATCCTTACCATCATCACAGATTCCCGAGCAGGTGAAGAAGGC  
TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTGTTCGCCAT  
GCTGTGCTTGCTCATCTTCTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTC  
ATGAAGCCAAAGGAGCCGATGACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGA  
GGACAGAACAACCTCCGAAGAAAAGAAAGAGTACTTCATCTAGATCAGCCTTTTTGTTTCAAT  
GAGGTGTCCAACCTGGCCCTATTTAGATGATAAAGAGACAGTGATATTGG

0944860 29844660

APPROVED	BY	CLASS	SUBCLASS

## FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518

<subunit 1 of 1, 440 aa, 1 stop

<MW: 48240, pI: 4.93, NX(S/T): 7

MASVVLPSPGSQCAAAAAAAPPGLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISC  
QVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQL  
YTDPPQESYTTITVLVPPRNLMDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKG  
KSEVEEWSDMYTVTSQMLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMT  
YPLQGLTREGDALELTCEAIGKPQPMVTVWRVDDMPQHAVLSGPNLFINNLNKTNDNGTYR  
CEASNIVGKAHSDYMLYVYDPPTTIPPTTTTTTTTTTTTTTTTTILTIIITDSRAGEEGSIRAVDH  
AVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEE  
KKEYFI

### Signal sequence.

amino acids 1-36

### Transmembrane domain.

amino acids 372-393

### N-glycosylation sites.

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,  
430-434

### Tyrosine kinase phosphorylation sites.

amino acids 233-240, 319-328

### N-myristoylation sites.

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,  
411-417, 427-433, 428-432

APPROVED BY	O.G. FIG.	
	CLASS	SUBCLASS
DRAFTSMAN		

00441862 003404



# FIGURE 25

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

094456-03101

GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCCGA  
 CCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCCGGCTCCCTGCGCCGCGCCGCGCTC  
 CCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT  
 GGGGCCTGGGGTGCAGGGCTGCCCATCCGGCTGCCAGTGCCAGCCAGCCACAGACAGTCTTCT  
 GCACTGCCCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTAC  
 GTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCTGCCGGGCCTGCA  
 GCTCCTGGACCTGTACAGAACCAGATCGCCAGCCTGCGCCTGCCCCGCTGCTGCTGCTGG  
 ACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAG  
 GCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGCG  
 CAACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAG  
 GCCTCCGGGGCCTGACGCGCCTGCGGCTGGCCGGCAACACCCGCATTGCCCAGCTGCGGCC  
 GAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGC  
 CCTGCCTGGCGACCTCTCGGGCCTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCGCAACC  
 CCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTACA  
 CTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCCGCCAAGAAGCTGGCCGGCTGCTCCT  
 GGAGCTTGACTACGCCGACTTTGGCTGCCAGCCACCACCACAGCCACAGTGCCACCA  
 CGAGGCCCGTGGTGCGGGAGCCACAGCCTTGTCTTAGCTTGGCTCCTACCTGGCTTAGC  
 CCCACAGCGCCGGCCACTGAGGCCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGC  
 TGTCCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGG  
 GGACACGGCACCACCTGGCGTGCTTGTGCCCCGAAGGCTTACGGGCCTGTACTGTGAGAGC  
 CAGATGGGGCAGGGGACACGGCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCT  
 GACCCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCC  
 AGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT  
 AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTGCG  
 GCCCAACGCCACTTACTCCGTCTGTGTGTCATGCCTTTGGGGCCCGGGCGGGTGCCGGAGGGCG  
 AGGAGGCTGCGGGGAGGCCCATACACCCAGCCGTCCACTCCAACCAGCCCCAGTCACC  
 CAGGCCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTGCTCCTGGC  
 CGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGGCGGGCCATGGCAGCAGCGG  
 CTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCCCTGGAAGTGGAGGGAGTGAAGGT  
 CCCTTGAGCCAGGCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCCAGCGGGTCTGA  
 GTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCACCCCTCCACGCAAAGC  
 CCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGC  
 CAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGA  
 CAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAG  
 ATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCAGAACCGAGTGCCATATGAGGACAGTGT  
 CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAAC  
 GCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCAGGCGGACCCTGGGGGCCAGTGAAGGAAG  
 CTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTCTAGTCTTGGCCCCAGG  
 AAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTAGGAACATGTTTTGCTTTTTTAA  
 AATATATATATTTATAAGAGATCCTTTCCCATTTATTCTGGGAAGATGTTTTTCAAATC  
 AGAGACAAGGACTTTGGTTTTTGTAAAGACAAACGATGATATGAAGGCCTTTTGTAAAGAAAA  
 ATAAAAAAAAAAAA

# FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVPLLLLPLLLLLLALGPGVQGCPSGCQCSQPQTTFCTARQGTTPRDPVPPDTVGLYVFEN  
GITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDANVEALRL  
AGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDLA  
GLAALQELDVSNLSLQALPGDLGSLFPRLRLAAARNPFNCVPLSWFGPWVRESHVTLASP  
EETRCHFPKPNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAP  
ATEAPSPSTAPPTVGPVPQPDCCPSTCLNGGTCHLGRHHLACLCPEGFTGLYCESQMGQ  
GTRPSPTPVTTPRPPRSLTLGIEPVSPSTSLRVGLQRYLQGSVQLRSLRLTYRNLSPDKRLV  
TLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQARE  
GNLPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAAQDKGQVGPAGPLELEGVKVPLEP  
GPKATEGGGEALPSGSECEVPLMGFPGLQSPHAKPYI

**Signal sequence.**

amino acids 1-23

**Transmembrane domain.**

amino acids 501-522

**N-glycosylation sites.**

amino acids 198-202, 425-429, 453-457

**Tyrosine kinase phosphorylation site.**

amino acids 262-270

**N-myristoylation sites.**

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**EGF-like domain cysteine pattern signature.**

amino acids 355-367

**Leucine zipper pattern.**

amino acids 122-144, 194-216

O.G. FIG.	SUBCLASS
	CLASS
APPROVED BY	DRAFTSMAN

094486-083101

# FIGURE 27

APPROVED BY DRAFTSMAN	O.G. FIG.	SUBCLASS
	CLASS	

FOI b7c 29344650

GGCACTAGGACAACCTTCTTCCCTTCTGCACCACTGCCCCGTACCCTTACCCGCCCCGCCACC  
 TCCTTGCTACCCCACTCTTGAAACCACAGCTGTTGGCAGGGTCCCCAGCTCATGCCAGCCTC  
 ATCTCCTTTCTTGCTAGCCCCCAAAGGGCCTCCAGGCAACATGGGGGGCCCAGTCAGAGAGC  
 CGGCACTCTCAGTTGCCCTCTGGTTGAGTTGGGGGGCAGCTCTGGGGGGCCGTGGCTTGTGCC  
 ATGGCTCTGCTGACCCAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA  
 GGGGACAGGAGGCCCCCTCCAGAATGGGGAAGGGTATCCCTGGCAGAGTCTCCCGGAGCAGA  
 GTTCCGATGCCCTGGAAGCCTGGGAGAATGGGGAGAGATCCCGGAAAAGGAGAGCAGTGCTC  
 ACCCAAAAACAGAAGAAGCAGCACTCTGTCCTGCACCTGGTTCCCATTAACGCCACCTCCAA  
 GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTTAGGCGTGGGAGAGGCCTAC  
 AGGCCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTTATCTGCTGTATAGCCAGGTC  
 CTGTTTCAAGACGTGACTTTACCATGGGTGAGGTGGTGTCTCGAGAAGGCCAAGGAAGGCA  
 GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCCACCCGGACCGGGCCTACAACAGCT  
 GCTATAGCGCAGGTGTCTTCCATTTACACCAAGGGGATATTCTGAGTGTCATAATTCCCCGG  
 GCAAGGGCGAACTTAACCTCTCTCCACATGGAACCTTCCTGGGGTTTGTGAAACTGTGATT  
 GTGTTATAAAAAGTGGCTCCCAGCTTGGAAGACCAGGGTGGGTACATACTGGAGACAGCCAA  
 GAGCTGAGTATATAAAGGAGAGGGAATGTGCAGGAACAGAGGCATCTTCCTGGGTTTGGCTC  
 CCCGTTCCCTCACTTTTCCCTTTTCATTCCCACCCCTAGACTTTGATTTTACGGATATCTTG  
 CTTCTGTTCCCCATGGAGCTCCG

## FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27433, pI: 9.85, NX(S/T): 2

MPASSPFLAPKGPNGMGGPVREPALSVALWLSWGAALGAVACAMALLTQOTELQSLRREV  
SRLQGTGGPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTQKQKKQHSVLHLVPIN  
ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREG  
QGRQETLFR CIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVII PRARAKLNLSPHGTFLGFVKL

**Signal sequence.**

amino acids 1-40

**N-glycosylation site.**

amino acids 124-128

**Tyrosine kinase phosphorylation site.**

amino acids 156-164

**N-myristoylation site.**

amino acids 36-42, 40-46, 179-185, 242-248

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 34-45

APPROVED BY	CLASS		SUBCLASS
	DRAFTSMAN		

FOI 29844660

# FIGURE 29

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

0944562-083101

CACTTTCTCCCTCTCTTCTTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGAC  
 CTCGGAGACCGCGCCGGGGAGACGGAGGTGCTGTGGGTGGGGGGACCTGTGGCTGCTCGTA  
 CCGCCCCCACCCTCCTCTTCTGCACTGCCGTCTCCGGAAGACCTTTTCCCCTGCTCTGTT  
 TCCTTCACCGAGTCTGTGCATCGCCCCGGACCTGGCCGGGAGGAGGCTTGGCCGGCGGGAGA  
 TGCTCTAGGGGCGGCGCGGGAGGAGCGGCCGGCGGGACGGAGGGCCCCGGCAGGAAGATGGGC  
 TCCCGTGGACAGGGACTCTTGCTGGCGTACTGCCTGCTCCTTGCCTTTGCCTCTGGCCTGGT  
 CCTGAGTCGTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC  
 CGTCGCCTCCGGACCATGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCCAGTCAG  
 GACCAGGGGCTCCCTGCTTCCCGGTGCTTGCCTGCTGTGACCCCGGTACCTCCATGTACCC  
 GGCGACCGCCGTGCCCCAGATCAACATCACTATCTTGAAAGGGGAGAAGGGTGACCGCGGAG  
 ATCGAGGCCTCCAAGGGAAATATGGCAAAACAGGCTCAGCAGGGGCCAGGGGCCACACTGGA  
 CCCAAAGGGCAGAAGGGCTCCATGGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC  
 CTTTTCGGTGGGCCGGAAGAAGCCCATGCACAGCAACCACTACTACCAGACGGTGATCTTCG  
 ACACGGAGTTCGTGAACCTCTACGACCACTTCAACATGTTACCGGCAAGTTCTACTGCTAC  
 GTGCCCGGCTCTACTTCTTCAACGTGCACACCTGGAACCAGAAGGAGACCTACCT  
 GCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTTTCGCGCAGGTGGGCGACCGCAGCA  
 TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACGCCTC  
 TACAAGGGCGAACGTGAGAACGCCATCTTCAGCGAGGAGCTGGACACCTACATCACCTTCAG  
 TGGCTACCTGGTCAAGCACGCCACCGAGCCCTAGCTGGCCGGCCACCTCCTTTCTCTCGCC  
 ACCTTCCACCCCTGCGCTGTGCTGACCCACCGCCTCTTCCCGATCCCTGGACTCCGACTC  
 CCTGGCTTTGGCATTCAAGTGAAGACGCCCTGCACACAGAAAGCCAAAGCGATCGGTGCTCC  
 CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAGGGCGGGGCACCCGC  
 GAGAACCCTCTGGGACCTTCCGCGGCCCTCTCTGCACACATCCTCAAGTGACCCCGCACGGC  
 GAGACGCGGGTGGCGGCAGGGCGTCCAGGGTGCGGCACCGCGGCTCCAGTCCCTGGAAATA  
 ATTAGGCAAATTCTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGG  
 TTGTTATTTTTGTCTTTCCAGCCAGCCTGCTGGCTCCCAAGAGAGAGGCCTTTTCAGTTGAG  
 ACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGGGTCAGGGGAGGGGCCGGGGCAGG  
 AAATACTCTGGCTTAATTCTTTTAAAGCCACGTAGGAACCTTCTTGAGGGATAGGTGGACC  
 CTGACATCCCTGTGGCCTTGCCCCAAGGGCTCTGCTGGTCTTTCTGAGTCACAGCTGCGAGGT  
 GATGGGGGCTGGGGCCCCAGGCGTCAGCCTCCAGAGGGACAGCTGAGCCCCCTGCCTTGGC  
 TCCAGGTTGGTAGAAGCAGCCGAAGGGCTCCTGACAGTGGCCAGGGACCCCTGGGTCCCCCA  
 GGCCTGCAGATGTTTCTATGAGGGGCAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC  
 ACCCTGTGCCACCCAGAGCCCTGGGGGGTGGTCTCCATGCCTGCCACCCTGGCATCGGCT  
 TTCTGTGCCGCTCCACACAAATCAGCCCCAGAAGGCCCGGGGCTTGGCTTCTGTTTTT  
 TATAAAACACCTCAAGCAGCACTGCAGTCTCCCATCTCCTCGTGGGCTAAGCATCACCGCTT  
 CCACGTGTGTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCACTGCCCT  
 CATCCAGGCCTCTGACCAGTAGCCTGAGAGGGGCTTTTTCTAGGCTTCAGAGCAGGGGAGAG  
 CTGGAAGGGGCTAGAAAGCTCCCGCTTGTCTGTTTTCTCAGGCTCCTGTGAGCCTCAGTCTG  
 AGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCCGTGTGAGGATCACTCTCAGGAGC  
 TGGGTGGCAGGAGAGGCAATAGCCCTGTGGCAATTGCAGGACCAGCTGGAGCAGGGTTGCG  
 GTGTCTCCACGGTGCTCTCGCCCTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCCC  
 ATAGCCCCCTCTCCACCTCACCCCATGTTGATGCCAGGGTCACTCTTGCTACCCGCTGGGCC  
 CCCAAACCCCGCTGCCTCTCTTCTTCCCCCATCCCCACCTGGTTTTGACTAATCCTGC  
 TTCCCTCTCTGGGCTGGCTGCCGGGATCTGGGGTCCCTAAGTCCCTCTCTTTAAAGAACTT  
 CTGCGGGTCAAGCTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGGAAGCAGAGCGCCACACTC  
 GCTGCTTAAGCTCCCCAGCTCTTTCAGAAAACATTAAACTCAGAATTGTGTTTTCAA

## FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234

><subunit 1 of 1, 281 aa, 1 stop

><MW: 31743, pI: 6.83, NX(S/T): 1

MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRP

SQDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGH

TGPKGQKGSMGAPGERCKSHYAAFVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFY

CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWV

RLYKGERENAIFSEELDTYITFSGYLVKHATEP

### Signal sequence.

amino acids 1-25

### N-glycosylation site.

amino acids 93-97

### N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

### Amidation site.

amino acids 150-154

### Cell attachment sequence.

amino acids 104-107

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

T07E90" 29844660

# FIGURE 31

APPROVED	O.G. FIG.	SUBCLASS
BY	CLASS	
DRAFTSMAN		

0944380-083104

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGCGGATTGCGCCGGTCCTTCCCCGCGG  
GCGCGACAGAGCTGTCCTCGCACCTGGATGGCAGCAGGGGCGCCGGGGTCCTCTCGACGCCA  
GAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAACCTAAGACCAAGAGGGAGGATTAT  
CCTTGACCTTTGAAGACCAAACTAAACTGAAATTTAAATGTTCTTCGGGGGAGAAGGGAG  
CTTGACTTACACTTTGGTAATAATTTGCTTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT  
GCCTCAAAAAGAGTCTAGAAGATGTTGTGTCATTGACATCCAGTCATCTCTTTCTAAGGGAATC  
AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTCTTGCTGTTCAAC  
AAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA  
GACAACCCAAGTCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA  
AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG  
CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAATTTTCAACAGCAGTCACTCCCC  
TAGCCCATCATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCT  
CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA  
GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTTACAATTTTCTCTGATCAAGAAA  
TAGCTCATCTGCTGCCTGAAAATGTGAGTGCGCTCCAGCTACGGTGGCAGTTGCTTCTCCA  
CATACCACCTCGGCTACTCCAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACC  
TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC  
AGCCTCCCACGACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG  
GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA  
AACCATACCGTTTACAGAAATCTCCAACCTTAACTTTGAACACAGGGAATGTGTATAACCTA  
CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTTGGGAAGGT  
AGGGAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCC  
ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTGTTGATAGGCC  
TCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT  
TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT  
TAGTAACCAGAAGCCCAAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG  
TATTTTGAAGACAGGAAAATGCCCCCTTCTGCTTCTCTTTTTTTTTTTGGAGACAGAGTCTT  
GCTCTGTTGCCAGGCTGGAGTGCACTAGCACGATCTCGGCTCTCACCGCAACCTCCGTCTC  
CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA  
CCACACCTGGGTGATTTTTGTATTTTTTAGTAGAGACGGGGTTTACCATGTTGGTCAGGCTG  
GTC'TCAAACCTCCTGACCTAGTGATCCACCCTCCTCGGCCTCCCAAAGTGCTGGGATTACAGG  
CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGAAGAAGGAATGAAGTG  
GGAACCAAATTAGGTAATTTTGGGTAATCTGTCTCTAAATATTAGCTAAAAACAAAGCTCT  
ATGTAAAGTAATAAAGTATAAATTGCCATATAAATTTCAAATTTCAACTGGCTTTTATGCAAA  
GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTCTTGGTTCCAGATAAAATCAAC  
TGTTTATATCAATTTCTAATGGATTTGCTTTTCTTTTATATGGATTCCTTTAAACTTATT  
CCAGATGTAGTTCCTTCCAATTAATATTGAATAAATCTTTTGTTACTCAA

## FIGURE 32

APPROVED BY DRAFTSMAN	O.G. FIG.	SUBCLASS
	CLASS	

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410

><subunit 1 of 1, 431 aa, 1 stop

><MW: 46810, pI: 6.45, NX(S/T): 6

MFFGGEGSLTYTLVIICFLTRLSASQNCLKKSLEDVVIDIQSSLKSGIRGNEPVYTSTQED  
 CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP  
 SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF  
 KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL  
 PTNASVTPSGTSQPQLATTAPPVTTVTSPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP  
 TDSKGSLETIPFTEISNLTGNTGNVYNPTALSMSNVESSTMNKTSWEGREASPGSSSQGSV  
 PENQYGLPFEKWWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSLDYLINGIYVDI

**Signal sequence.**

amino acids 1-25

**Transmembrane domain.**

amino acids 384-405

**N-glycosylation sites.**

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 415-419

**Tyrosine kinase phosphorylation site.**

amino acids 50-57

**N-myristoylation sites.**

amino acids 4-10, 48-54, 315-321

FOI 880-29874660



# FIGURE 33

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

GCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC  
 GCCTCCTTGTGTGCCTGGTATTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT  
 GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCCTCAAAGCTCCAGTCC  
 CCAAAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA  
 CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG  
 AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAACCTGGGA  
 ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG  
 TTTATTCAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC  
 AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA  
 TGAAATTCAGGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAACCTCCCTTCCGAAATT  
 CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGA  
 GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTGACACTGCAGGGTCCTGAGTAAAT  
 GTGTTCTGTATAAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCAACA  
 GCCCATATTTGATGAGTATTTTGGGTTTGTGTAAACCAATGAACATTTGCTAGTTGTATCA  
 AATCTTGGTACGCAGTATTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA  
 AACTAAAATGAATGGAAATTCTTAAAAAAAAA

294460  
 294460  
 294460

# FIGURE 34

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777

><subunit 1 of 1, 235 aa, 1 stop

><MW: 25982, pI: 9.09, NX(S/T): 2

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK  
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT  
RCFDMYEGDNSGPMTKFIQSAAPKSLLFMVTDGSTRLNNDKNAIEALGSKEIRNMKFRS  
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

101E80-29844650